R. Hutson

RAW SEQUENCE LISTING DATE: 12/20/2002
PATENT APPLICATION: **US/09/512,019** TIME: 11:07:58

Input Set : **N:\Crf3\RULE60\09512019.raw**
Output Set: **N:\CRF4\12202002\I512019.raw**

ENTERED

<110> APPLICANT: HONG, GUOFAN
HUANG, WEI-HUA
<120> TITLE OF INVENTION: DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE SELECTIVE DISCRIMINATION AGAINST FLUORESCENT DYE-LABELED DIDEOXYNUCLEQTIDES
<130> FILE REFERENCE: hongsequencelisting
<140> CURRENT APPLICATION NUMBER: 09/512,019
<141> CURRENT FILING DATE: 2000-02-24
<150> PRIOR APPLICATION NUMBER: US/09/157,397
<151> PRIOR FILING DATE: 1998-09-21
<150> PRIOR APPLICATION NUMBER: 08/544,643
<151> PRIOR FILING DATE: 1995-10-18
<150> PRIOR APPLICATION NUMBER: 08/642,684
<151> PRIOR FILING DATE: 1996-05-03
<160> NUMBER OF SEQ ID NOS: 11
<170> SOFTWARE: PatentIn Ver. 2.0 - beta
<210> SEQ ID NO: 1
<211> LENGTH: 1764
<212> TYPE: DNA
<213> ORGANISM: Bacillus stearothermophilus
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gccccgattg tcggaatcgc actagtgaac gagcatgggc gatttttat gcgcccggag 180
accgcgctgg ctgattcgca atttttagca tggcttgccg atgaaacgaa gaaaaaaagc 240
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atcgctgcgg tggcgaaaat gaaacaatat gaagcggtgc ggtcggatga agcggtctat 420
ggcaaaggcg tcaagcggtc gctgccggac gaacagacgc ttgctgagca tctcgttcgc 480
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ttcgccgccg attactcaca aattgaattg cgcgtcctcg cccatatcgc cgatgacgac 1140
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aaagaagctg ccgaatttat cgaacgttac ttcgccagct ttccgggcgt aaagcagtat 1380
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cgccgctatt tgcctgatat tacaagccgc aatttcaacg tccgcagttt tgcagagcgg 1500
acggccatga acacgccaat tcaaggaagc gccgctgaca ttattaaaaa agcgatgatt 1560
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<212> TYPE: PRT
<213> ORGANISM: Bacillus stearothermophilus
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20 25 30
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45
Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu Ala
50 55 60
Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65 70 75 80
Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly Ile
85 90 95
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110
Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met Lys
115 120 125
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Val
130 135 140
Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val Arg
145 150 155 160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
165 170 175
Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu His Ala Leu
180 185 190
Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr
195 200 205
Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220
Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255
Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
260 265 270
Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
275 280 285

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100       Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
101       305                 310                 315                 320
102       Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
103                       325                 330                 335
104       Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
105                   340                 345                 350
106       Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
107               355                 360                 365
108       Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
109           370                 375                 380
110       Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
111       385                 390                 395                 400
112       Phe Gln Leu Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
113                       405                 410                 415
114       Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
115                   420                 425                 430
116       Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
117               435                 440                 445
118       Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
119           450                 455                 460
120       Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
121       465                 470                 475                 480
122       Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
123                       485                 490                 495
124       Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
125                   500                 505                 510
126       Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
127               515                 520                 525
128       Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
129           530                 535                 540
130       Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Glu Leu Val Pro
131       545                 550                 555                 560
132       Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
133                       565                 570                 575
134       Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
135                   580                 585
137 <210> SEQ ID NO: 3
138 <211> LENGTH: 1764
139 <212> TYPE: DNA
140 <213> ORGANISM: Bacillus stearothermophilus
141 <400> SEQUENCE: 3
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143       gaagagatgc ttgccgacaa ggcagcgctt gtcgttgagg tgatggaaga aaactaccac 120
144       gatgccccga ttgtcggaat cgcactagtg aacgagcatg ggcgattttt tatgcgcccg 180
145       gagaccgcgc tggctgattc gcaattttta gcatggcttg ccgatgaaac gaagaaaaaa 240
146       agcatgtttg acgccaagcg ggcagtcgtt gccttaaagt ggaaaggaat tgagcttcgc 300
147       ggcgtcgcct ttgatttatt gctcgctgcc tatttgctca atccggctca agatgccggc 360
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148        gatatcgctg cggtggcgaa aatgaaacaa tatgaagcgg tgcggtcgga tgaagcggtc 420
149        tatggcaaag gcgtcaagcg gtcgctgccg gacgaacaga cgcttgctga gcatctcgtt 480
150        cgcaaagcgg cagccatttg ggcgcttgag cagccgttta tggacgattt gcggaacaac 540
151        gaacaagatc aattattaac gaagcttgag cacgcgctgg cggcgatttt ggctgaaatg 600
152        gaattcactg gggtgaacgt ggatacaaag cggcttgaac agatgggttc ggagctcgcc 660
153        gaacaactgc gtgccatcga gcagcgcatt tacgagctag ccggccaaga gttcaacatt 720
154        aactcaccaa aacagctcgg agtcatttta tttgaaaagc tgcagctacc ggtgctgaag 780
155        aagacgaaaa caggctattc gacttcggct gatgtgcttg agaagcttgc gccgcatcat 840
156        gaaatcgtcg aaaacatttt gcattaccgc cagcttggca aactgcaatc aacgtatatt 900
157        gaaggattgt tgaaagttgt gcgccctgat accggcaaag tgcatacgat gttcaaccaa 960
158        gcgctgacgc aaactgggcg gctcagctcg gccgagccga acttgcaaaa cattccgatt 1020
159        cggaccccac tggggcggaa aatccgccaa gcgttcgtcc cgtcagagcc ggactggctc 1080
160        attttcgccg ccgattactc acaaattgaa ttgcgcgtcc tcgcccatat cgccgatgac 1140
161        gacaatctaa ttgaagcgtt ccaacgcgat ttggatattc acacaaaaac ggcgatggac 1200
162        attttccagt tgagcgaaga ggaagtcacg gccaacatgc gccgccaggc aaaggccgtt 1260
163        aactacggta tcgtttacgg aattagcgat tacggattgg cgcaaaactt gaacattacg 1320
164        cgcaaagaag ctgccgaatt tatcgaacgt tacttcgcca gctttccggg cgtaaagcag 1380
165        tatatggaaa acatagtgca agaagcgaaa cagaaaggat atgtgacaac gctgttgcat 1440
166        cggcgccgct atttgcctga tattacaagc cgcaatttca acgtccgcag ttttgcagag 1500
167        cggacggcca tgaacacgcc aattcaagga agcgccgctg acattattaa aaaagcgatg 1560
168        attgatttag cggcacggct gaaagaagag cagcttcagg ctcgtctttt gctgcaagtg 1620
169        catgacgagc tcattttgga agcgccaaaa gaggaaattg agcgattatg tgagcttgtt 1680
170        ccggaagtga tggagcaggc cgttacgctc cgcgtgccgc tgaaagtcga ctaccattac 1740
171        ggcccaacat ggtatgatgc caaa                                       1764
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174 <211> LENGTH: 588
175 <212> TYPE: PRT
176 <213> ORGANISM: Bacillus stearothermophilus
177 <400> SEQUENCE: 4
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180        Asp Val Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val
181                     20                  25                  30
182        Glu Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala
183                 35                  40                  45
184        Leu Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu
185             50                  55                  60
186        Ala Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys
187         65                  70                  75                  80
188        Ser Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly
189                         85                  90                  95
190        Ile Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu
191                    100                 105                 110
192        Leu Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met
193                115                 120                 125
194        Lys Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly
195            130                 135                 140
196        Val Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val
197        145                 150                 155                 160
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```
198  Arg Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp
199                  165                 170                 175
200  Leu Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu His Ala
201              180                 185                 190
202  Leu Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp
203          195                 200                 205
204  Thr Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg
205      210                 215                 220
206  Ala Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile
207  225                 230                 235                 240
208  Asn Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu
209                  245                 250                 255
210  Pro Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val
211              260                 265                 270
212  Leu Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His
213          275                 280                 285
214  Tyr Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu
215      290                 295                 300
216  Lys Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln
217  305                 310                 315                 320
218  Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln
219                  325                 330                 335
220  Asn Ile Pro Ile Arg Thr Pro Leu Gly Arg Lys Ile Arg Gln Ala Phe
221              340                 345                 350
222  Val Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln
223          355                 360                 365
224  Ile Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile
225      370                 375                 380
226  Glu Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp
227  385                 390                 395                 400
228  Ile Phe Gln Leu Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln
229                  405                 410                 415
230  Ala Lys Ala Val Asn Tyr Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly
231              420                 425                 430
232  Leu Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile
233          435                 440                 445
234  Glu Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn
235      450                 455                 460
236  Ile Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His
237  465                 470                 475                 480
238  Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg
239                  485                 490                 495
240  Ser Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala
241              500                 505                 510
242  Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys
243          515                 520                 525
244  Glu Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu
245      530                 535                 540
246  Ile Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Glu Leu Val
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VERIFICATION SUMMARY DATE: 12/20/2002
PATENT APPLICATION: **US/09/512,019** TIME: 11:07:59

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